



-1-

SEQUENCE LISTING

<110> Gray et al.

<120> MACROPHAGE DERIVED CHEMOKINE (MDC), MDC ANALOGS, MDC
INHIBITOR SUBSTANCES, AND USES THEREOF

<130> 27866/34810

<140> 09/509,165

<141> 2000-06-12

<150> 09/067,447

<151> 1998-04-28

<150> 08/939,107

<151> 1997-09-26

<150> 08/660,542

<151> 1996-06-07

<150> 08/558,658

<151> 1995-11-16

<150> 08/479,620

<151> 1995-06-07

<160> 46

<170> PatentIn Ver. 2.0

<210> 1

<211> 2923

<212> DNA

<213> Homo sapiens - human MDC cDNA

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<222> (92)..(298)

<400> 1

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Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val

-20

-15

ctc gtc ctc ctt gct gtg gcg ctt caa gca act gag gca ggc ccc tac 100

Leu Val Leu Leu Ala Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr

-10

-5

1

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MAR 12 2002

TECH CENTER 1600/2900

ggc gcc aac atg gaa gac agc gtc tgc tgc cgt gat tac gtc cgt tac 148
Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr
5 10 15

cgt ctg ccc ctg cgc gtg gtg aaa cac ttc tac tgg acc tca gac tcc 196
Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser
20 25 30 35

tgc ccg agg cct ggc gtg gtg ttg cta acc ttc agg gat aag gag atc 244
Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile
40 45 50

tgt gcc gat ccc aga gtg ccc tgg gtg aag atg att ctc aat aag ctg 292
Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu
55 60 65

agc caa tgaagagcct actctgatga ccgtggcctt ggctcctcca ggaaggctca 348
Ser Gln

ggagccctac ctccctgccca ttatagctgc tccccgccag aagcctgtgc caactctctg 408

cattccctga tctccatccc tgtggctgtc acccttggtc acctccgtgc tgtcactgcc 468

atctcccccc tgaccctct aaccatcct ctgcctccct cctgcagtc agagggctct 528

gttcccatca gcgattcccc tgcttaaacc cttocatgac tccccactgc cctaagctga 588

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caatgggtgtg gtcttggtt attgaagcct ctgcctcctg ggttcaagt attctcttgc 1308

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<211> 93
<212> PRT
<213> Homo sapiens - human MDC

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 -20 -15 -10

Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu
 -5 -1 1 5

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg
 10 15 20

Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
 25 30 35 40

Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg
 45 50 55

Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
 60 65

<210> 3
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer JHSP6

<400> 3
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<210> 4
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer M13

<400> 4
gtaaaacgac ggccagt 17

<210> 5
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer T3.1

<400> 5

aattaaccct cactaaaggg

20

<210> 6

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer T7.1

<400> 6

gtaatagcgc tcactatagg gc

22

<210> 7

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390-1F

<400> 7

tctatctaga ggcccctacg gcgccaacat ggaag

35

<210> 8

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390-2R

<400> 8

caccggatcc tcattggctc agcttattga gaa

33

<210> 9

<211> 29

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer 390-4R

<400> 9

aatggatcca cagcacggag gtgaccaag

29

<210> 10
<211> 31
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer 390-3R

<400> 10
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<210> 11
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-FX2

<400> 11
tatcggatcc tggttccgcg tggcccctac ggcgccaaca tggaa 45

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer GEX5

<400> 12
gaaatccagc aagtatatag ca 22

<210> 13
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-Pe1

<400> 13
attgccatgg ccggccccta cggcgccaac atggaa 36

<210> 14
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390RcH

<400> 14

gaccaagctt gagacataca ggacagagca

30

<210> 15

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390RcX

<400> 15

tg gatctaga agttggcaca ggcttctgg

29

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer DC03

<400> 16

cgaaattaat acgactcact

20

<210> 17

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer
390mycRX

<400> 17

tg gatctaga tcaattcaag tctcctcgc tgatcagctt ctgctcttgg ctcagcttat 60

tgagaat

67

<210> 18

<211> 99

<212> PRT

<213> Homo sapiens - Hu MCP-3

<400> 18

Met Lys Ala Ser Ala Ala Leu Leu Cys Leu Leu Leu Thr Ala Ala Ala
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Phe Ser Pro Gln Gly Leu Ala Gln Pro Val Gly Ile Asn Thr Ser Thr
-5 1 5

Thr Cys Cys Tyr Arg Phe Ile Asn Lys Lys Ile Pro Lys Gln Arg Leu
10 15 20 25

Glu Ser Tyr Arg Arg Thr Thr Ser Ser His Cys Pro Arg Glu Ala Val
30 35 40

Ile Phe Lys Thr Lys Leu Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln
45 50 55

Lys Trp Val Gln Asp Phe Met Lys His Leu Asp Lys Lys Thr Gln Thr
60 65 70

Pro Lys Leu
75

<210> 19

<211> 99

<212> PRT

<213> Homo sapiens - Hu MCP-1

<400> 19

Met Lys Val Ser Ala Ala Leu Leu Cys Leu Leu Leu Ile Ala Ala Thr
-20 -15 -10

Phe Ile Pro Gln Gly Leu Ala Gln Pro Asp Ala Ile Asn Ala Pro Val
-5 1 5

Thr Cys Cys Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu
10 15 20 25

Ala Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val
30 35 40

Ile Phe Lys Thr Ile Val Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln
45 50 55

Lys Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr
60 65 70

Pro Lys Thr
75

<210> 20

<211> 76

<212> PRT

<213> Homo sapiens - Hu MCP-2

<400> 20

Gln Pro Asp Ser Val Ser Ile Pro Ile Thr Cys Cys Phe Asn Val Ile
1 5 10 15

Asn Arg Lys Ile Pro Ile Gln Arg Leu Glu Ser Tyr Thr Arg Ile Thr
20 25 30

Asn Ile Gln Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Lys Arg Gly
35 40 45

Lys Glu Val Cys Ala Asp Pro Lys Glu Arg Trp Val Arg Asp Ser Met
50 55 60

Lys His Leu Asp Gln Ile Phe Gln Asn Leu Lys Pro
65 70 75

<210> 21

<211> 91

<212> PRT

<213> Homo sapiens - RANTES

<400> 21

Met Lys Val Ser Ala Ala Ala Leu Ala Val Ile Leu Ile Ala Thr Ala
-20 -15 -10

Leu Cys Ala Pro Ala Ser Ala Ser Pro Tyr Ser Ser Asp Thr Thr Pro
-5 1 5

Cys Cys Phe Ala Tyr Ile Ala Arg Pro Leu Pro Arg Ala His Ile Lys
10 15 20 25

Glu Tyr Phe Tyr Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val Phe
30 35 40

Val Thr Arg Lys Asn Arg Gln Val Cys Ala Asn Pro Glu Lys Lys Trp
45 50 55

Val Arg Glu Tyr Ile Asn Ser Leu Glu Met Ser
60 65

<210> 22

<211> 91

<212> PRT

<213> Homo sapiens - MIP-1 beta

<400> 22

Met Lys Leu Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala
-20 -15 -10

Phe Cys Ser Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr
-5 1 5

Ala Cys Cys Phe Ser Tyr Thr Arg Glu Ala Ser Ser Asn Phe Val Val
10 15 20 25

Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val Phe
30 35 40

Gln Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser Trp
45 50 55

Val Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn
60 65

<210> 23

<211> 92

<212> PRT

<213> Homo sapiens - MIP-1 alpha

<400> 23

Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala
-20 -15 -10

Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala
-5 1 5 10

Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala
15 20 25

Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe
30 35 40

Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp
45 50 55

Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala
60 65 70

<210> 24

<211> 96

<212> PRT

<213> Homo sapiens - I-309

<400> 24

Met Gln Ile Ile Thr Thr Ala Leu Val Cys Leu Leu Leu Ala Gly Met
-20 -15 -10

Trp Pro Glu Asp Val Asp Ser Lys Ser Met Gln Val Pro Phe Ser Arg
-5 1 5 10

Cys Cys Phe Ser Phe Ala Glu Gln Glu Ile Pro Leu Arg Ala Ile Leu
15 20 25

Cys Tyr Arg Asn Thr Ser Ser Ile Cys Ser Asn Glu Gly Leu Ile Phe
30 35 40

Lys Leu Lys Arg Gly Lys Glu Ala Cys Ala Leu Asp Thr Val Gly Trp
45 50 55

Val Gln Arg His Arg Lys Met Leu Arg His Cys Pro Ser Lys Arg Lys
60 65 70

<210> 25

<211> 93

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human MDC Analog

<220>

<221> misc_feature

<222> (24)

<223> Xaa = arg, gly, ala, val, leu, ile,
pro, ser, thr, phe, tyr, trp, aspartate,
glutamate, asn, gln, cys, or met

<220>

<221> misc_feature

<222> (27)

<223> Xaa = lys, gly, ala, val, leu, ile, pro, ser, thr, phe, tyr, trp,
aspartate, glutamate, asn, gln, cys, or met

<220>

<221> misc_feature

<222> (30)

<223> Xaa = tyr, ser, lys, arg, his, aspartate, glutamate, asn, gln, or
cys

<220>

<221> misc_feature

<222> (50)

<223> Xaa = glu, lys, arg, his, gly, or ala

<220>
<221> misc_feature
<222> (59)
<223> Xaa = trp, ser, lys, arg, his, aspartate, glutamate, asn, gln, or
cys

<220>
<221> misc_feature
<222> (60)
<223> Xaa = val, ser, lys, arg, his, aspartate, glutamate, asn, gln, or
cys

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-20 -15 -10

Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu
-5 1 5

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Xaa
10 15 20

Val Val Xaa His Phe Xaa Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
25 30 35 40

Val Val Leu Leu Thr Phe Arg Asp Lys Xaa Ile Cys Ala Asp Pro Arg
45 50 55

Val Pro Xaa Xaa Lys Met Ile Leu Asn Lys Leu Ser Gln
60 65

<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 390-7F

<400> 26
tattggatcc gttctagctc cctgttctcc

30

<210> 27
<211> 31
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 390-8R

<400> 27

ccaagaattc ctgcagccac tttctgggct c

31

<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer ARA1

<400> 28

gcgactctct actgtttctc

20

<210> 29

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer ARA2

<400> 29

cacaggaaac agctatgacc

20

<210> 30

<211> 70

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human MDC analog

<400> 30

Leu Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp
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Tyr Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp
20 25 30

Thr Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg
35 40 45

Asp Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile
50 55 60

Leu Asn Lys Leu Ser Gln
65 70

<210> 31
<211> 69
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human MDC analog

<400> 31

Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr
1 5 10 15

Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr
20 25 30

Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp
35 40 45

Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Tyr Leu Lys Met Ile Leu
50 55 60

Asn Lys Leu Ser Gln
65

<210> 32
<211> 69
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human MDC analog

<400> 32

Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr
1 5 10 15

Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys Glu Tyr Phe Tyr Thr
20 25 30

Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp
35 40 45

Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu
50 55 60

Asn Lys Leu Ser Gln
65

<210> 33
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 <212> DNA
 <213> Homo sapiens - human CCR4 cDNA

<220>
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 agaaaagcaa gctgcttctg gttgggcca gacctgcctt gaggagcctg tagagttaaa 180

aa atg aac ccc acg gat ata gca gat acc acc ctc gat gaa agc ata 227
 Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile
 1 5 10 15

tac agc aat tac tat ctg tat gaa agt atc ccc aag cct tgc acc aaa 275
 Tyr Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys
 20 25 30

gaa ggc atc aag gca ttt ggg gag ctc ttc ctg ccc cca ctg tat tcc 323
 Glu Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser
 35 40 45

ttg gtt ttt gta ttt ggt ctg ctt gga aat tct gtg gtg gtt ctg gtc 371
 Leu Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val
 50 55 60

ctg ttc aaa tac aag cgg ctc agg tcc atg act gat gtg tac ctg ctc 419
 Leu Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu
 65 70 75

aac ctt gcc atc tcg gat ctg ctc ttc gtg ttt tcc ctc cct ttt tgg 467
 Asn Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp
 80 85 90 95

ggc tac tat gca gca gac cag tgg gtt ttt ggg cta ggt ctg tgc aag 515
 Gly Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys
 100 105 110

atg att tcc tgg atg tac ttg gtg ggc ttt tac agt ggc ata ttc ttt 563
 Met Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe
 115 120 125

gtc atg ctc atg agc att gat aga tac ctg gcg ata gtg cac gcg gtg 611
 Val Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val
 130 135 140

ttt tcc ttg agg gca agg acc ttg act tat ggg gtc atc acc agt ttg	659
Phe Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu	
145 150 155	
gct aca tgg tca gtg gct gtg ttc gcc tcc ctt cct ggc ttt ctg ttc	707
Ala Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe	
160 165 170 175	
agc act tgt tat act gag cgc aac cat acc tac tgc aaa acc aag tac	755
Ser Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr	
180 185 190	
tct ctc aac tcc acg acg tgg aag gtt ctc agc tcc ctg gaa atc aac	803
Ser Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn	
195 200 205	
att ctc gga ttg gtg atc ccc tta ggg atc atg ctg ttt tgc tac tcc	851
Ile Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser	
210 215 220	
atg atc atc agg acc ttg cag cat tgt aaa aat gag aag aag aac aag	899
Met Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys	
225 230 235	
gcg gtg aag atg atc ttt gcc gtg gtg gtc ctc ttc ctt ggg ttc tgg	947
Ala Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp	
240 245 250 255	
aca cct tac aac ata gtg ctc ttc cta gag acc ctg gtg gag cta gaa	995
Thr Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu	
260 265 270	
gtc ctt cag gac tgc acc ttt gaa aga tac ttg gac tat gcc atc cag	1043
Val Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln	
275 280 285	
gcc aca gaa act ctg gct ttt gtt cac tgc tgc ctt aat ccc atc atc	1091
Ala Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile	
290 295 300	
tac ttt ttt ctg ggg gag aaa ttt cgc aag tac atc cta cag ctc ttc	1139
Tyr Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe	
305 310 315	
aaa acc tgc agg ggc ctt ttt gtg ctc tgc caa tac tgt ggg ctc ctc	1187
Lys Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu	
320 325 330 335	
caa att tac tct gct gac acc ccc agc tca tct tac acg cag tcc acc	1235
Gln Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr	
340 345 350	

atg gat cat gat ctt cat gat gct ctg taggaaaaat gaaatggtga 1282
Met Asp His Asp Leu His Asp Ala Leu
355 360

aatgcagagt caatgaactt ttccacattc agagcttact ttaaaattgg tatttttagg 1342
taagagatcc ctgagccagt gtcaggagga aggettacac ccacagtga aagacagctt 1402
ctcatcctgc aggcagcttt ttctctccca ctagacaagt ccagcctggc aagggttcac 1462
ctgggctgag gcatccttcc tcacaccagg cttgcctgca ggcattgagtc agtctgatga 1522
gaactctgag cagtgttga atgaagttgt aggtaatat gcaaggcaaa gactattccc 1582
ttctaacctg aactgatggg ttctccaga gggaattgca gactactggc tgatggagta 1642
aatcgctacc ttttgctgtg gcaaattggc ccccg 1677

<210> 34
<211> 360
<212> PRT
<213> Homo sapiens - human CCR4

<400> 34
Met Asn Pro Thr Asp Ile Ala Asp Thr Thr Leu Asp Glu Ser Ile Tyr
1 5 10 15
Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu
20 25 30
Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu
35 40 45
Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu
50 55 60
Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn
65 70 75 80
Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly
85 90 95
Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met
100 105 110
Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val
115 120 125
Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
130 135 140

Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala
145 150 155 160

Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser
165 170 175

Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser
180 185 190

Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile
195 200 205

Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met
210 215 220

Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala
225 230 235 240

Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp Thr
245 250 255

Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val
260 265 270

Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala
275 280 285

Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr
290 295 300

Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys
305 310 315 320

Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln
325 330 335

Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr Met
340 345 350

Asp His Asp Leu His Asp Ala Leu
355 360

<210> 35

<211> 1784

<212> DNA

<213> murine MDC cDNA

<220>

<221> CDS

<222> (1) .. (276)

<220>

<221> mat_peptide

<222> (73)..(276)

<400> 35

atg tct aat ctg cgt gtc cca ctc ctg gtg gct ctc gtc ctt ctt gct	48
Met Ser Asn Leu Arg Val Pro Leu Leu Val Ala Leu Val Leu Leu Ala	
-20 -15 -10	

gtg gca att cag acc tct gat gca ggt ccc tat ggt gcc aat gtg gaa	96
Val Ala Ile Gln Thr Ser Asp Ala Gly Pro Tyr Gly Ala Asn Val Glu	
-5 1 5	

gac agt atc tgc tgc cag gac tac atc cgt cac cct ctg cca tca cgt	144
Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His Pro Leu Pro Ser Arg	
10 15 20	

tta gtg aag gag ttc ttc tgg acc tca aaa tcc tgc cgc aag cct ggc	192
Leu Val Lys Glu Phe Phe Trp Thr Ser Lys Ser Cys Arg Lys Pro Gly	
25 30 35 40	

gtt gtt ttg ata acc gtc aag aac cga gat atc tgt gcc gat ccc agg	240
Val Val Leu Ile Thr Val Lys Asn Arg Asp Ile Cys Ala Asp Pro Arg	
45 50 55	

cag gtc tgg gtg aag aag cta ctc cat aaa ctg tcc tagggaggag	286
Gln Val Trp Val Lys Lys Leu Leu His Lys Leu Ser	
60 65	

gacctgatga ccatgggtct ggtgtggtcc agggaggctc agcaagccct attcttctgc 346

cattccagca agagccttgc caacgacgcc acctttactc acctccatcc cctgggctgt 406

cactctgtca ggctctggtc cctctacctc cctctatcc cttccagctt atcccccttc 466

aatgtggcag ctgggaacaa cattcaggcc agccttacct aatgcctact cccactgct 526

ttagatgaga ccagcgtcct tgttttgatg ccctgatcct atgatgcctt ccccatcccc 586

agccttggcc cctttctctt cttgcatgta gggaaggccc ataggtttca aatatgtgct 646

acctacttcc ctttctgggg ggttctaata ccagcatgt ttttctgct gcaggcacct 706

atccagtgcc acacacctcc caagtttcta tcagtcccag tgggcatcca ccaagcccca 766

aacttcagac ttccttggcc tccacctact ctcatgagaa ttctgggagt ttcaggctgg 826

tccaccaggc cccccagggt taggccaagg tccccaccag agctcctcct gtttcttggt 886

ctgcagcacg gggcaggagg caaggagcag gtcagaatc agatttctta aaggagctgc 946

agactccatc agtaaaagga atctttctcc catcctgaa tataaggcag ttttctgtca 1006

acacagagac tcaggttggt agaaatggcc acatagatca actgtgaaac cctaaattta 1066
ccaagaatca acttccaccc ctcttcaacc acatgctagg gtcttttact ttctctgccc 1126
cacacctttg actccttgcc tgtgtagctg atagtcgaag ttatgctatg gtgtcagtga 1186
ctgccacagt ttgtttggta ttataagcta tagttatatt tatataggaa agaggataaa 1246
tatatgtggg ccaaatagac gaactggaga gtttttaggat ctggggggcag gaagggccat 1306
acaaagtgat acctcagaaa atagatgggt gtgggagctg ctgccagtgg cagagttaac 1366
ttaaagaact taattgaaat tattcttgag tggtgagggc caagacaaga atatagaacc 1426
cattcttgct tccctggaga caacagtggc cccaggggaa ggaataaacc ttcttgctcc 1486
tctggagggg gcatggcctg rcttagccga gtgactggac tgtgtgagat tgggggcatc 1546
gcttttctcy tctgagcctc agctgacagc atatgggacc acaaagggtg tgatccaaac 1606
cacagggatt gacagtgccg gccacagctg tgtccagggc tctgtgttctg ccagaaggag 1666
cacctggacg accagggcca ccactagtgc tactttgctc actgccccatg catgtcctga 1726
aggtccctcc cctctctctc ctacttctgg gaaaataaat gctcgccaat aatacctg 1784

<210> 36
<211> 92
<212> PRT
<213> murine MDC

<400> 36
Met Ser Asn Leu Arg Val Pro Leu Leu Val Ala Leu Val Leu Leu Ala
-20 -15 -10

Val Ala Ile Gln Thr Ser Asp Ala Gly Pro Tyr Gly Ala Asn Val Glu
-5 1 5

Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His Pro Leu Pro Ser Arg
10 15 20

Leu Val Lys Glu Phe Phe Trp Thr Ser Lys Ser Cys Arg Lys Pro Gly
25 30 35 40

Val Val Leu Ile Thr Val Lys Asn Arg Asp Ile Cys Ala Asp Pro Arg
45 50 55

Gln Val Trp Val Lys Lys Leu Leu His Lys Leu Ser
60 65

<210> 37
<211> 958
<212> DNA
<213> rat MDC cDNA


<220>
<221> CDS
<222> (1)..(243)

<220>
<221> mat_peptide
<222> (40)..(243)

<220>
<221> misc_feature
<222> (206)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (785)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (827)
<223> n = A or G or T or C

 <220>
<221> misc_feature
<222> (836)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (861)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (864)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (871)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (878)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (206)
<223> n = A or G or T or C

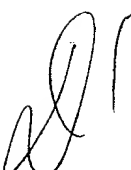
<220>
<221> misc_feature
<222> (882)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (900)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (902)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (206)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (907)
<223> n = A or G or T or C

 <220>
<221> misc_feature
<222> (206)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (916)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (921)
<223> n = A or G or T or C

<220>
<221> misc_feature
<222> (951)
<223> n = A or G or T or C

<220>

<221> misc_feature

<222> (958)

<223> n = A or G or T or C

<400> 37

ctc gtc ctt ctt gct gtg gca ctt cag acc tcc gat gca ggt ccc tat 48
Leu Val Leu Leu Ala Val Ala Leu Gln Thr Ser Asp Ala Gly Pro Tyr
-10 -5 1

ggt gcc aat gtg gaa gac agt atc tgc tgc cag gac tac atc cgt cac 96
Gly Ala Asn Val Glu Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His
5 10 15

cct ctg cca cca cgt ttc gtg aag gag ttc tac tgg acc tca aag tcc 144
Pro Leu Pro Pro Arg Phe Val Lys Glu Phe Tyr Trp Thr Ser Lys Ser
20 25 30 35

tgc cgc aag cct ggc gtc gtt ttg ata acc atc aag aac cga gat atc 192
Cys Arg Lys Pro Gly Val Val Leu Ile Thr Ile Lys Asn Arg Asp Ile
40 45 50

tgt gct gac ccc ang atg ctc tgg gtg aag aag ata ctc cac aag ttg 240
Cys Ala Asp Pro Xaa Met Leu Trp Val Lys Lys Ile Leu His Lys Leu
55 60 65

gcc tagggagaag ggccctgatga ccacgggtct ggtgtctcca caaggctcag 293
Ala

caaaccctat ccttctgccca tccagcaaga gccttgccaa caactccacc tttgctcacc 353

tccatccctt ggggtgtcac tctgtgaagc ctggggtccc tgtacttctt gtccgtcccc 413

tccagctcat tctcttccaa cgtggcagcc gggaagcact tctggctagc cttaccaat 473

actactcccc actgctttaa atgagaccag ggtccttggt ttggtgcctt tggatcctat 533

gatgccttcc cagtctccag ccttggcccc cttctcttct tacatgtagg gaacaccaat 593

atctttcaag tatgtgttac ccaattcttc ttcctcggag gctgctggga cccggaatat 653

tatccctgc tgcaggcctc tccaagcacc actcacctcc caggctttcc atccgtccca 713

gtcccaagcc ccatgcttca gaacttcctt tggtcccccc ctacactcca caaattctgg 773

ggaagtctca cnaactgggt cccctcaggc cccacggga aggaaggctc cccnccaaca 833

acntcctctt gttttccccg gtctcccncc nccgggantt gggcnccna atcccccaatt 893

tctgaanang aacngcccat tcntcccntt aaaattaacc tttccccccc tccctgangt 953

taggn 958

<210> 38
<211> 81
<212> PRT
<213> rat

<220>
<221> misc_feature
<222> (56)
<223> Xaa = any or unknown amino acid

<400> 38
Leu Val Leu Leu Ala Val Ala Leu Gln Thr Ser Asp Ala Gly Pro Tyr
 -10 -5 1


Gly Ala Asn Val Glu Asp Ser Ile Cys Cys Gln Asp Tyr Ile Arg His
 5 10 15

Pro Leu Pro Pro Arg Phe Val Lys Glu Phe Tyr Trp Thr Ser Lys Ser
20 25 30 35

Cys Arg Lys Pro Gly Val Val Leu Ile Thr Ile Lys Asn Arg Asp Ile
 40 45 50

Cys Ala Asp Pro Xaa Met Leu Trp Val Lys Lys Ile Leu His Lys Leu
 55 60 65

Ala

 <210> 39
<211> 506
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: S. cerevisiae alpha factor pre-
 pro/human MDC cDNA chimeric construct

<220>
<221> CDS
<222> (15)..(476)

<220>
<221> mat_peptide
<222> (270)..(476)

<400> 39
atctcgagct cacg atg aga ttt cct tca att ttt act gca gtt tta ttc 50
 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe
 -85 -80 -75

gca gca tcc tcc gca tta gct gct cca gtc aac act aca aca gaa gat	98
Ala Ala Ser Ser Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp	
-70 -65 -60	
gaa acg gca caa att ccg gct gaa gct gtc atc ggt tac tta gat tta	146
Glu Thr Ala Gln Ile Pro Ala Glu Ala Val Ile Gly Tyr Leu Asp Leu	
-55 -50 -45	
gaa ggg gat ttc gat gtt gct gtt ttg cca ttt tcc aac agc aca aat	194
Glu Gly Asp Phe Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn	
-40 -35 -30	
aac ggg tta ttg ttt ata aat act act att gcc agc att gct gct aaa	242
Asn Gly Leu Leu Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys	
-25 -20 -15 -10	
gaa gaa ggg gta cct ttg gat aaa aga ggc ccc tac ggc gcc aac atg	290
Glu Glu Gly Val Pro Leu Asp Lys Arg Gly Pro Tyr Gly Ala Asn Met	
-5 1 5	
gaa gac agc gtc tgc tgc cgt gat tac gtc cgt tac cgt ctg ccc ctg	338
Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu	
10 15 20	
cgc gtg gtg aaa cac ttc tac tgg acc tca gac tcc tgc ccg agg cct	386
Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro	
25 30 35	
ggc gtg gtg ttg cta acc ttc agg gat aag gag atc tgt gcc gat ccc	434
Gly Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro	
40 45 50 55	
aga gtg ccc tgg gtg aag atg att ctc aat aag ctg agc caa	476
Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln	
60 65	
tgaaggcctt ctagagcggc cgcacgcata	506

<210> 40
 <211> 154
 <212> PRT
 <213> cDNA

<400> 40
 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
 -85 -80 -75 -70
 Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
 -65 -60 -55

Ile Pro Ala Glu Ala Val Ile Gly Tyr Leu Asp Leu Glu Gly Asp Phe
-50 -45 -40

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
-35 -30 -25

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
-20 -15 -10

Pro Leu Asp Lys Arg Gly Pro Tyr Gly Ala Asn Met Glu Asp Ser Val
-5 1 5 10

Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg Val Val Lys
15 20 25

His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly Val Val Leu
30 35 40

Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg Val Pro Trp
45 50 55

Val Lys Met Ile Leu Asn Lys Leu Ser Gln
60 65

<210> 41

<211> 93

<212> FRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human MDC Analog

<220>

<221> misc_feature

<222> (2)

<223> Xaa = not proline

<400> 41

Met Ala Arg Leu Gln Thr Ala Leu Leu Val Val Leu Val Leu Leu Ala
-20 -15 -10

Val Ala Leu Gln Ala Thr Glu Ala Gly Xaa Tyr Gly Ala Asn Met Glu
-5 1 5

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg
10 15 20

Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
25 30 35 40

Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg
45 50 55

Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
60 65

<210> 42
<211> 538
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (53)..(334)

<220>
<221> mat_peptide
<222> (122)..(334)

<400> 42
ccctgagcag agggacctgc acacagagac tccctcctgg gctcctggca cc atg gcc 58
Met Ala

cca ctg aag atg ctg gcc ctg gtc acc ctc ctc ctg ggg gct tct ctg 106
Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Leu Gly Ala Ser Leu
-20 -15 -10

cag cac atc cac gca gct cga ggg acc aat gtg ggc cgg gag tgc tgc 154
Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu Cys Cys
-5 1 5 10

ctg gag tac ttc aag gga gcc att ccc ctt aga aag ctg aag acg tgg 202
Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys Thr Trp
15 20 25

tac cag aca tct gag gac tgc tcc agg gat gcc atc gtt ttt gta act 250
Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe Val Thr
30 35 40

gtg cag ggc agg gcc atc tgt tcg gac ccc aac aac aag aga gtg aag 298
Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg Val Lys
45 50 55

aat gca gtt aaa tac ctg caa agc ctt gag agg tct tgaagcctcc 344
Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser
60 65 70

tcaccccaga ctctgactg tctcccggga ctacctggga cctccaccgt tgggtgttcac 404

cgccccacc ctgagcgctt ggggtccaggg gaggccttcc agggacgaag aagagccaca 464

gtgagggaga tcccatcccc ttgtctgaac tggagccatg ggcacaaagg gccagatta 524
aagtctttat cctc 538

<210> 43
<211> 94
<212> PRT
<213> Homo sapiens

<400> 43
Met Ala Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Leu Gly Ala
-20 -15 -10
Ser Leu Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu
-5 1 5
Cys Cys Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys
10 15 20 25
Thr Trp Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe
30 35 40
Val Thr Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg
45 50 55
Val Lys Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser
60 65 70

<210> 44
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 44
atgggaccat atggagcaaa tatggaagat agt 33

<210> 45
<211> 335
<212> DNA
<213> Macaque MDC

<220>
<221> CDS
<222> (19) .. (297)

<400> 45

agacatacag gacagagc atg gct cgc cta cag act gtg ttc ctg ggt gtc 51
Met Ala Arg Leu Gln Thr Val Phe Leu Gly Val
-20 -15

ctc atc ctc ctt gct gtg gcg ctt caa gca act gag gca ggc ccc tat 99
Leu Ile Leu Leu Ala Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr
-10 -5 1

ggc gcc aac atg gaa gac agc gtc tgc tgc cgt gat tac gtc cgt tac 147
Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr
5 10 15

cgt atg ccc ctg cgt gtg gtg aaa cac ttc tac tgg acc tca gac tcc 195
Arg Met Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser
20 25 30 35

tgc ccg agg cct ggc gtg gtg ttg cta acc tcc agg gat aag gag atc 243
Cys Pro Arg Pro Gly Val Val Leu Leu Thr Ser Arg Asp Lys Glu Ile
40 45 50

tgt gcc gat ccc aga gtg ccc tgg gtg aag atg att ctc aat aag ctg 291
Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu
55 60 65

agc caa tgaagagcct actatgatga ccgtggccta agcaagcc 335
Ser Gln

<210> 46

<211> 93

<212> PRT

<213> Macaque MDC

<400> 46

Met Ala Arg Leu Gln Thr Val Phe Leu Gly Val Leu Ile Leu Leu Ala
1 5 10 15

Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr Gly Ala Asn Met Glu
20 25 30

Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Met Pro Leu Arg
35 40 45

Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser Cys Pro Arg Pro Gly
50 55 60

Val Val Leu Leu Thr Ser Arg Asp Lys Glu Ile Cys Ala Asp Pro Arg
65 70 75 80

Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu Ser Gln
85 90

advised